

RESULT 1

BCDO_CHICK

ID BCDO_CHICK STANDARD; PRT; 526 AA.
AC Q9I993;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta,beta-carotene 15,15'-dioxygenase (EC 1.14.99.36) (Beta-carotene
DE dioxygenase 1).
GN BCDO.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=LSL Lohmann; TISSUE=Duodenum;
RX MEDLINE=20261261; PubMed=10799297;
RA Wyss A., Wirtz G.M., Woggon W.D., Brugger R., Wyss M., Friedlein A.,
RA Bachmann H., Hunziker W.;
RT "Cloning and expression of beta,beta-carotene-15,15'-dioxygenase.";
RL Biochem. Biophys. Res. Commun. 271:334-336(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LSL Lohmann; TISSUE=Duodenum;
RX MEDLINE=21134366; PubMed=11237856;
RA Wyss A., Wirtz G.M., Woggon W.D., Brugger R., Wyss M., Friedlein A.,
RA Riss G., Bachmann H., Hunziker W.;
RT "Expression pattern and localization of beta,beta-carotene 15,15'-
RT dioxygenase in different tissues.";
RL Biochem. J. 354:521-529(2001).
CC -!- FUNCTION: Symmetrically cleaves beta-carotene into two molecules
CC of retinal. The reaction proceeds in three stages, epoxidation of
CC the 15,15'-double bond, hydration of the double bond leading to
CC ring opening, and oxidative cleavage of the diol formed.
CC -!- CATALYTIC ACTIVITY: Beta-carotene + O(2) = 2 retinal.
CC -!- COFACTOR: Iron.
CC -!- PATHWAY: Vitamin A biosynthesis.
CC -!- SIMILARITY: Belongs to the beta-carotene dioxygenase family.
CC -----
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CC -----
DR EMBL; AJ271386; CAB90825.1; -.
DR InterPro; IPR004294; RPE65.
DR Pfam; PF03055; RPE65; 1.
KW Dioxygenase; Oxidoreductase; Iron.
SQ SEQUENCE 526 AA; 60384 MW; 82C6EAAF75FE345B CRC64;

Query Match 100.0%; Score 2825; DB 1; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.4e-191;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 METIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSF 60
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Db      1 METIFNRNKEEHPEPIKAEVQGQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSF 60

Qy     61 TFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDCKNIFAKAFSYLSHTIPEF 120
      |||
Db     61 TFKNGEVYYRSKYLRSDTYNCNIEANRIVVSEFGTMAYPDCKNIFAKAFSYLSHTIPEF 120

Qy    121 TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGN 180
      |||
Db    121 TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGN 180

Qy    181 ILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCIPSRSLLQPSYYHSFGI 240
      |||
Db    181 ILNMGTSIVDKGRTKYVLFKIPSSVPEKEKKKSCFKHLEVVCIPSRSLLQPSYYHSFGI 240

Qy    241 TENYIVFIEQPFKLDIVKLATAYIRGVNWSCLSFHKEDKTWFHFVDRKTKKEVSTKFYT 300
      |||
Db    241 TENYIVFIEQPFKLDIVKLATAYIRGVNWSCLSFHKEDKTWFHFVDRKTKKEVSTKFYT 300

Qy    301 DALVLYHHINAYEEDGHVVFDDIVAYRDNSLYDMFYLLKKLDKDFEVNNKLTSTIPTCKRFVV 360
      |||
Db    301 DALVLYHHINAYEEDGHVVFDDIVAYRDNSLYDMFYLLKKLDKDFEVNNKLTSTIPTCKRFVV 360

Qy    361 PLQYDKDAEVGSNLVKLPTSATAVKEKDGSIIYCQPEILCEGIELPRVNYDYGKKYKYVY 420
      |||
Db    361 PLQYDKDAEVGSNLVKLPTSATAVKEKDGSIIYCQPEILCEGIELPRVNYDYGKKYKYVY 420

Qy    421 ATEVQWSPVPTKIAKLNVTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTCTVVVSE 480
      |||
Db    421 ATEVQWSPVPTKIAKLNVTKEVLHWGEDHCWPSEPIFVPSPDAREEDEGVVLTCTVVVSE 480

Qy    481 PNKAPFLLILDAKTFKELGRATVNVEMHLDLHGMFIPQNDLGAETE 526
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Db    481 PNKAPFLLILDAKTFKELGRATVNVEMHLDLHGMFIPQNDLGAETE 526
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RESULT 1

Q7ZTS0

ID Q7ZTS0 PRELIMINARY; PRT; 516 AA.
AC Q7ZTS0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bcdol protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049331; AAH49331.1; -.
DR InterPro; IPR004294; RPE65.
DR Pfam; PF03055; RPE65; 1.
SQ SEQUENCE 516 AA; 58655 MW; DFBAC7D058736E53 CRC64;

Query Match 60.9%; Score 1720; DB 13; Length 516;
Best Local Similarity 59.9%; Pred. No. 3.7e-123;
Matches 311; Conservative 86; Mismatches 114; Indels 8; Gaps 5;

Qy 1 METIFNRNKEEHPEPIKAQVQQLPTWLQGVLLRNGPGMHTIGDTKYNHWFDGLALLHSF 60
|: : :||| ||||| ||:| :| :||| :||| ||| :||| :||| ||||| :||| |||||
Db 1 MQDYDGKNKEEHPEPIKTEVKGSIPQEWVQGTILRNGPGMFSVGETTYNHWFDGMALLHSF 60
Qy 61 TFKNGEVYYRSKYLRSDTYNCNIEANRIVSEFGTMAPDPCKNIFAKAFSYLSHTIPEF 120
||| |||: ||| ||||| ||: ||||| ||||| ||||| ||||| :| :||| ||||| :

Db 61 AINKGEVTYRSRYLRGDTYNSNMQANRIVVSEMGTMAYPDPCKNIFSKVITFLSHTIPDF 120
 Qy 121 TDNCLINIMKTGDDYYATSETNFIRKIDPQTLETLDKVDYSKYVAVNLATSHPHYDSAGN 180
 |||| |::| |:::|||||:||||| |||| :|:| ||: |: : || ||| ||
 Db 121 TDNCGNNIIKYGNDFHATSETNYIRKIDPVTLETQEKIDYLYLKYLPVSIVASHTHYDKEGN 180
 Qy 181 ILNMGTSIVDKGRTKYVLFKIP-SSVPEKEKKKSCFKHLEVVCIPSRSLLQPSYYHSFG 239
 :||| | :||:||||:||||: | | : | | :| |||| |||||
 Db 181 SYSMGTICIAEKGKTKYMLFKVPGESRPDGSP---LKSAEAVCTLPCRSLLTPSYYSFG 237
 Qy 240 ITENYIVFIEQPFKLDIVKLATAYIRGVNWASCLSFHKEDKTWFHFVDRKTKKEVSTKFY 299
 :|:| | :||| | |||:|:||||: | :|||: || || | | :|| |||||:|
 Db 238 MTDNYFIFIEQPLKLDILKMATAYLRRVSWASCMKFHPEDSTLIHLIDRNTKKEVATKFY 297
 Qy 300 TDALVLYHHINAYEEDGHVVFDIVAYRDNLSLYDMFYLLKKLDKDFEVNNKLTSIPTCKRFV 359
 |||: :| | :||:|:|||||:|:| | | :| | | : | | | |
 Db 298 TDAMTVYHQVNAFEDDGHVVFDVIAYDDNNLYEFFYLNKLKETMGATN-LYCKPKFTRFV 356
 Qy 360 VPLQYDKDAEVGSNLVKLP-TSATAVKEKDGSICYQPEILCEGIELPRVNYDYGKKYKY 418
 || | | |||| |:|:||||| | || | :|||:||||:|:|:|
 Db 357 FPL--SDQGETGENLVKLKYTTASAVKEKDGMQGEVLCEGVLPRIYNFNNGKKYRY 414
 Qy 419 VYATEVQWSPVPTKIAKLVQTKVLEHWGEDHCWPSEPIFVPSPDAREEDEGVVLTVCVVV 478
 | | ||| |:| | : ||: : | | : |||:|:| | | :||:| ||| :
 Db 415 SYMCCVDESPVATRIVKFDADTKQIEWKGGDFASEPVFIPRPGAVDEDDGVVLTVIIN 474
 Qy 479 SEPNAKAPLLILDAKTFKELGRATVNVEMHLDLHGMFIP 517
 :| : |||:||||:|:| | :|:|:|:| |
 Db 475 NKPLQGGFLLVLDKSFKEIARACLDVEIHMDMHGYFIP 513